

Figure 1A  
Identification of Functional Allele Families:  
Motivation

◆ Repetitive Gene Systems

- Repetitive Biochemical Functions
- E.g. systems 1, 7

◆ Both systems must be inactivated  
before problems

- E.g. (( $1A_2$  or  $1B_3$ ) and ( $7A_3$  or  $7C_1$ ))
- Automatic choice of allele  
combinations required

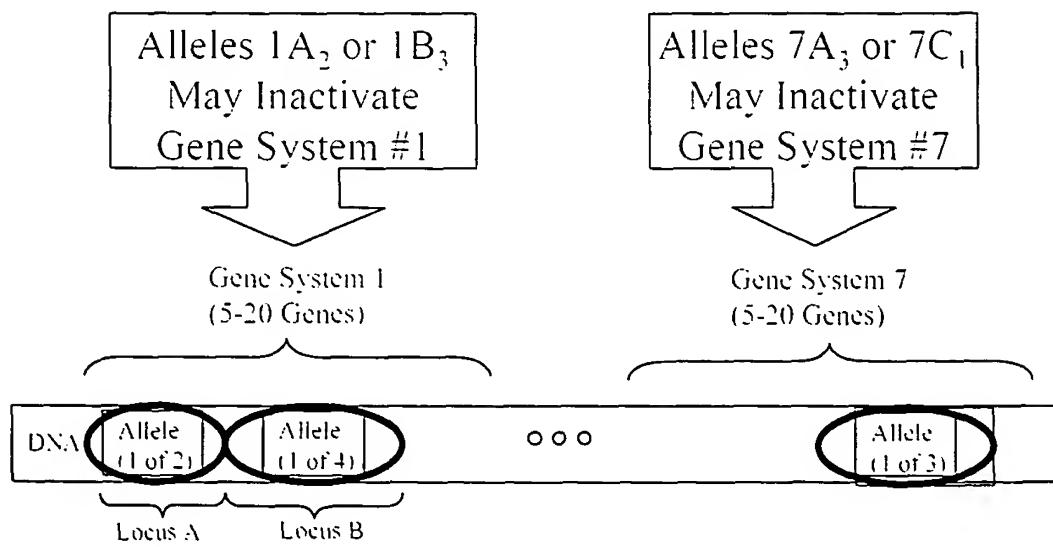


Figure 1B  
Method of Identifying Clinically Relevant  
Allele Combinations

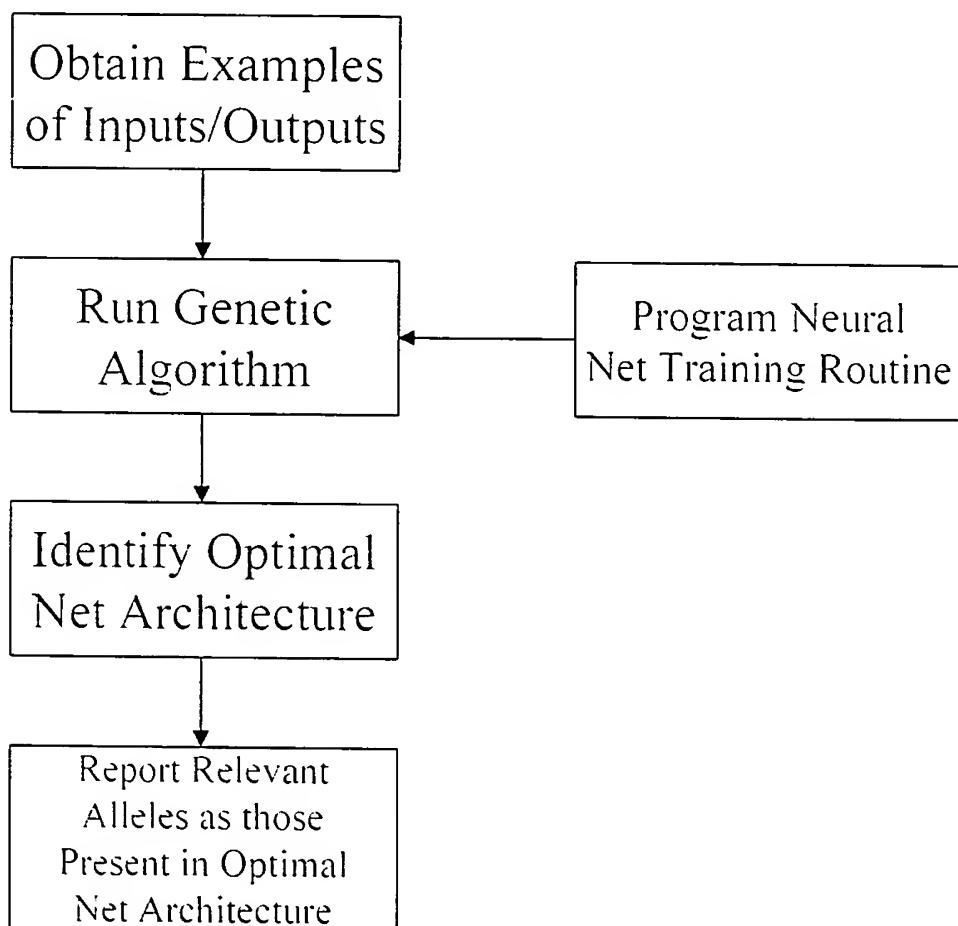


Figure 1C  
Structure of Neural Network  
Training Routine

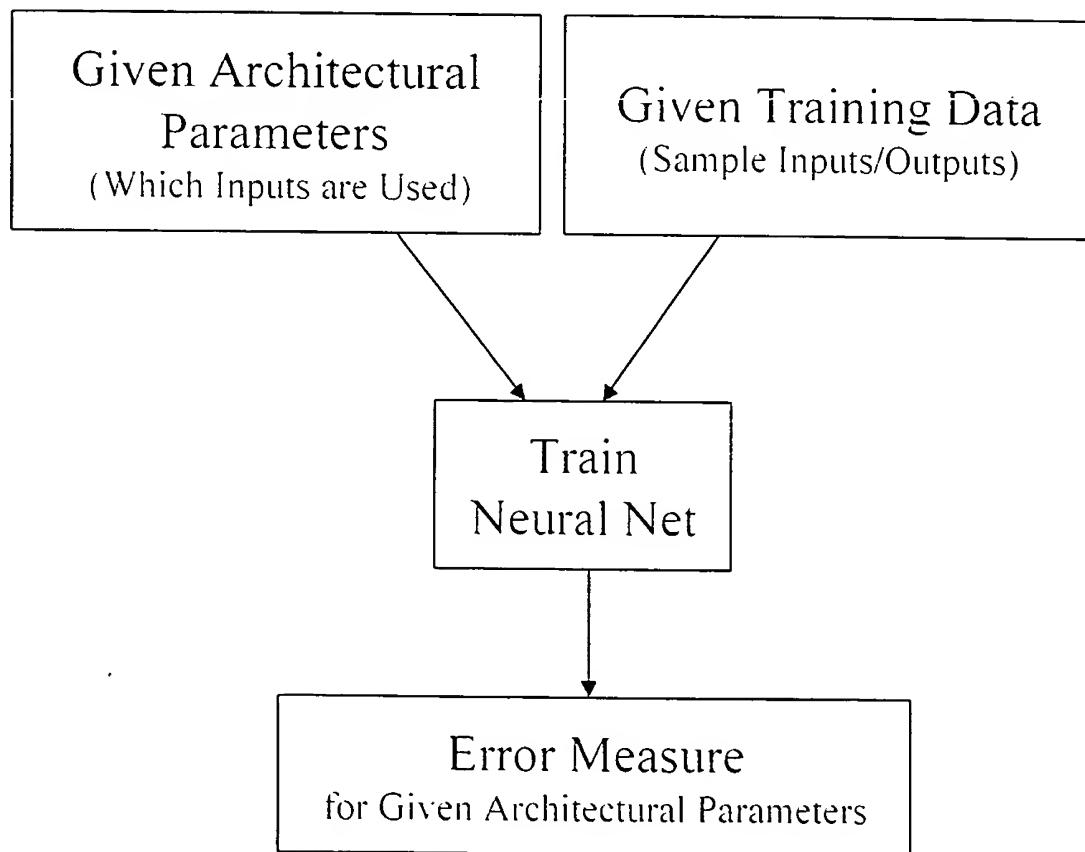


Figure 1D:  
Typical Mapping Neural Network

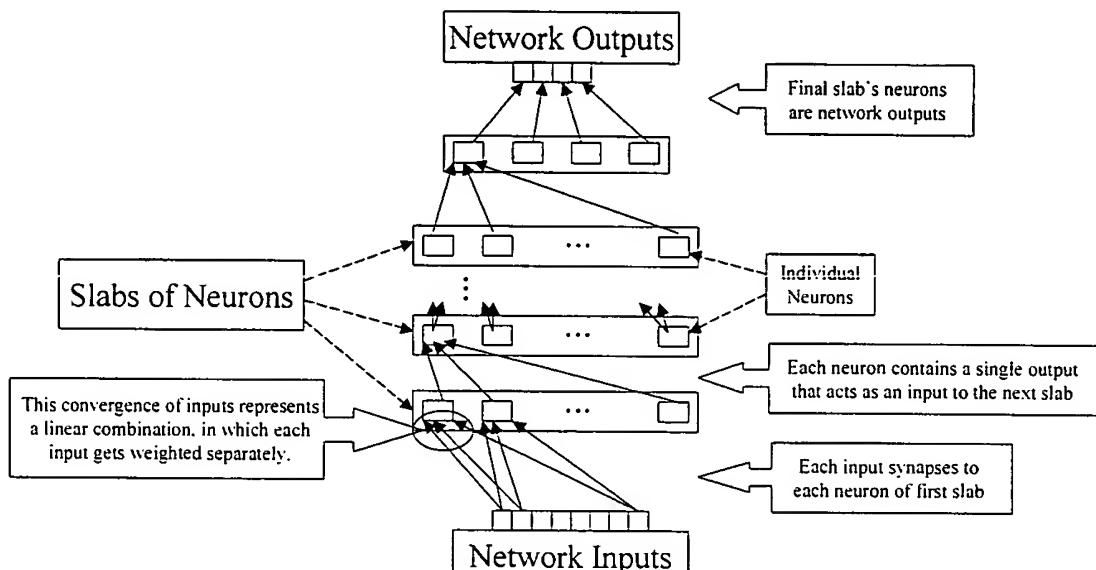


Figure 1E: Typical Genetic Algorithm

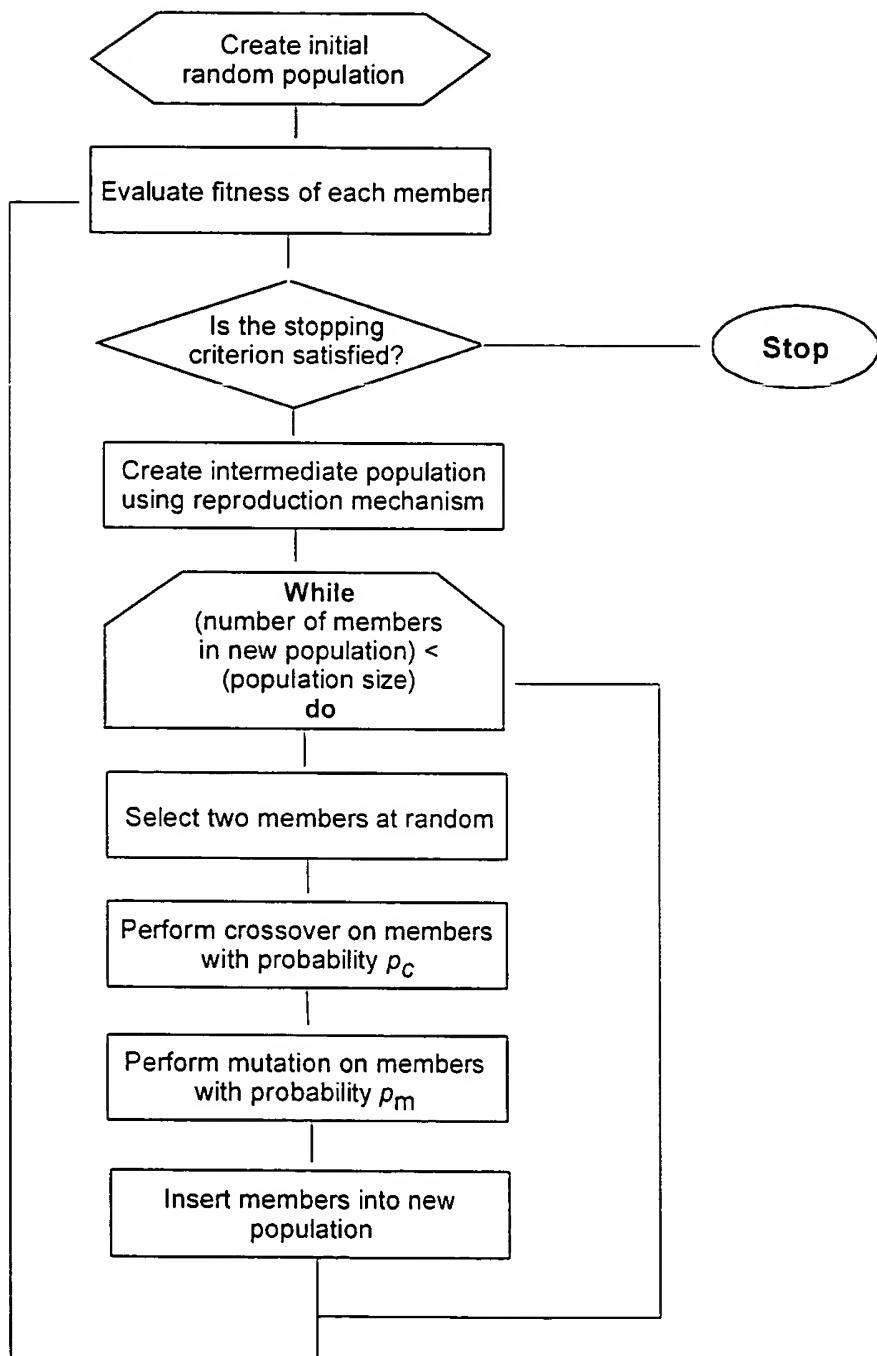


Figure 2  
Method of Predicting Clinical Variables  
Given Genomic Data

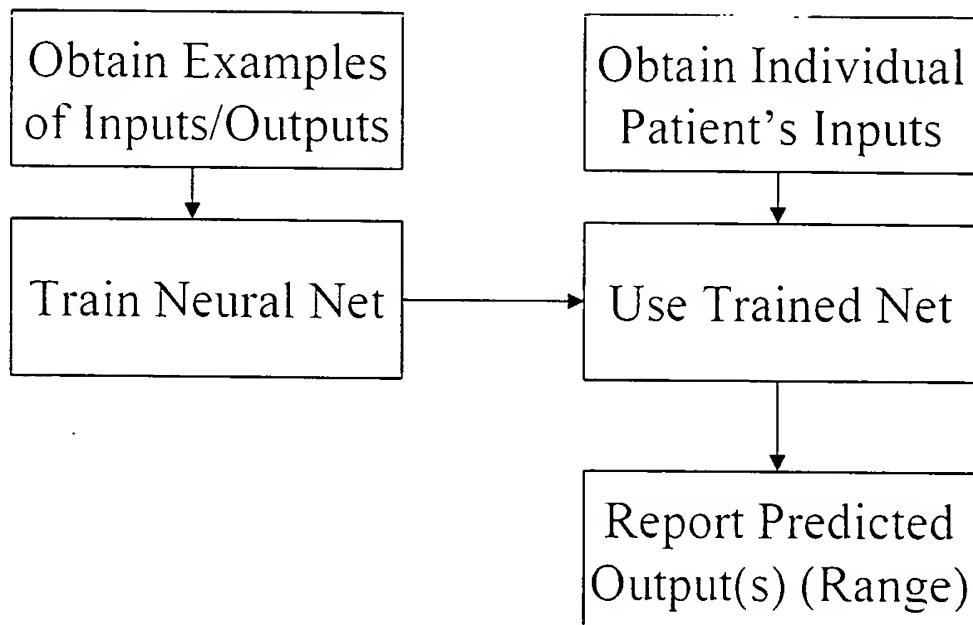


Figure 3  
Genomic Methods of Screening Patients for  
Clinical Drug Use

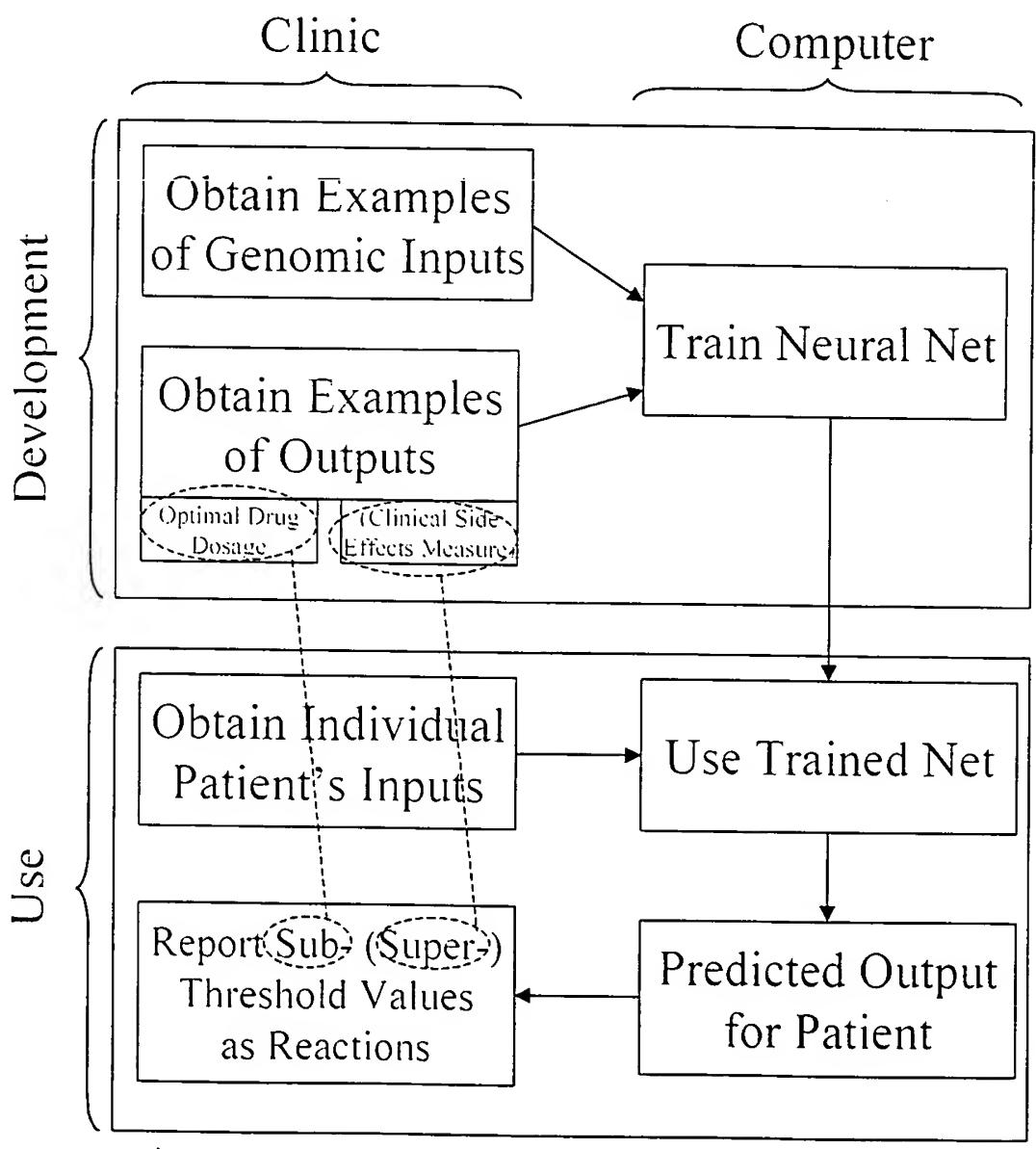


Figure 4A  
GA Rolling: Illustration of Infeasible Initial  
Mapping Problem

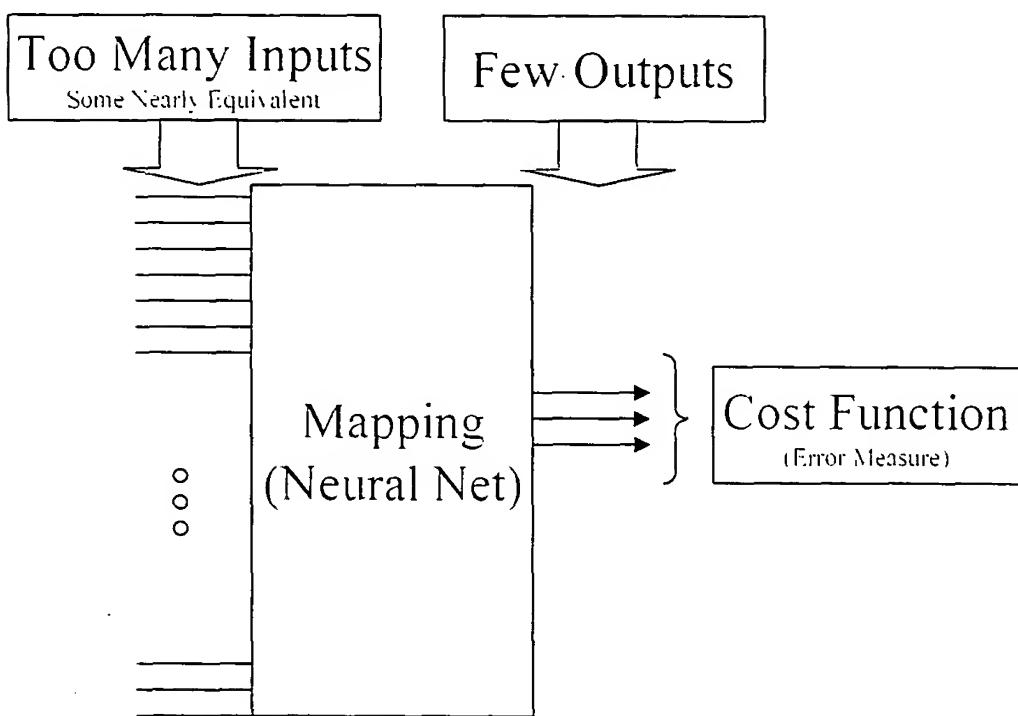


Figure 4B  
GA Rolling: Illustration of Individual Category and its Genes

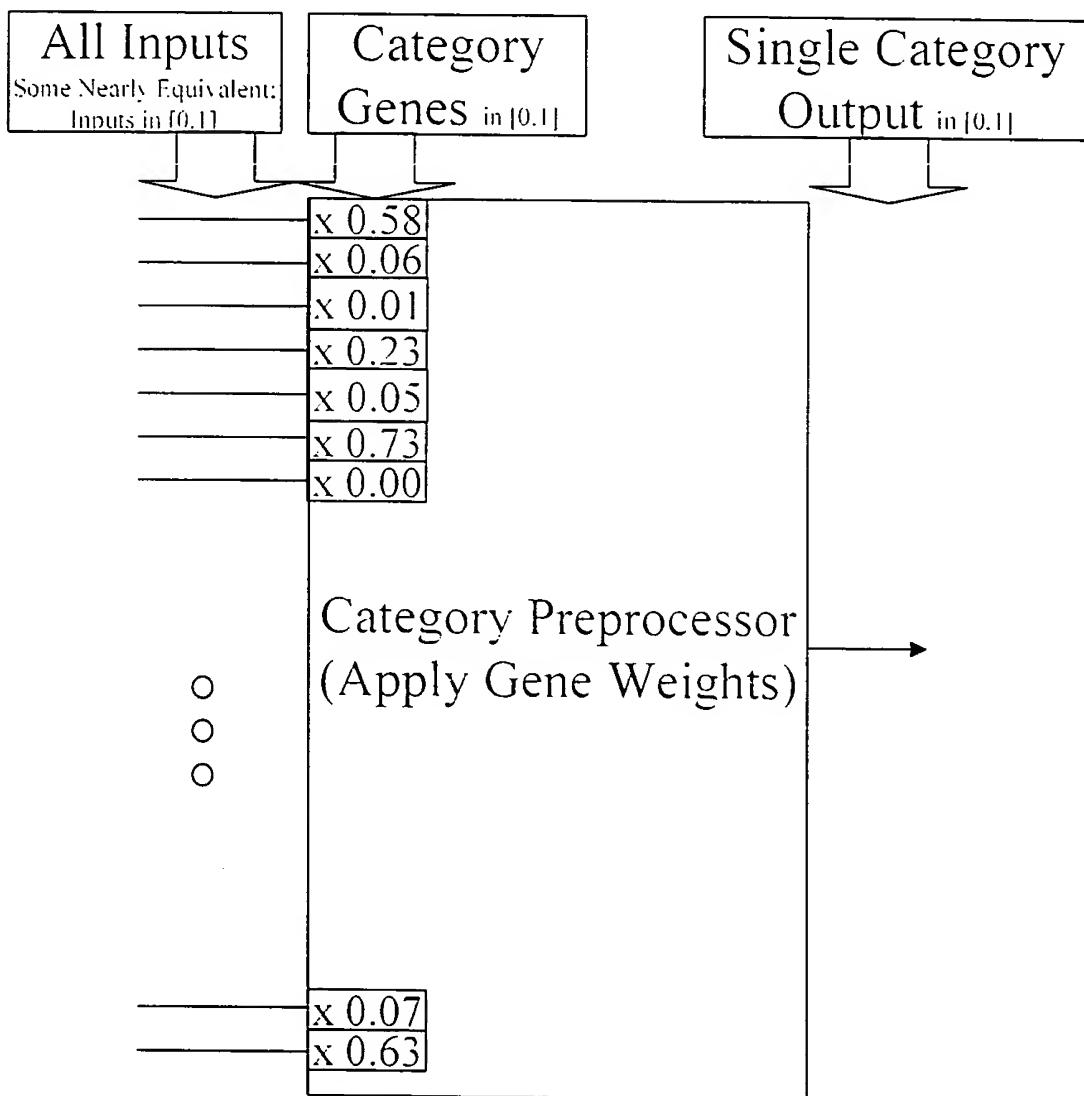


Figure 4C  
GA Rolling: Illustration of the Mapping  
Used by the Genetic Algorithm

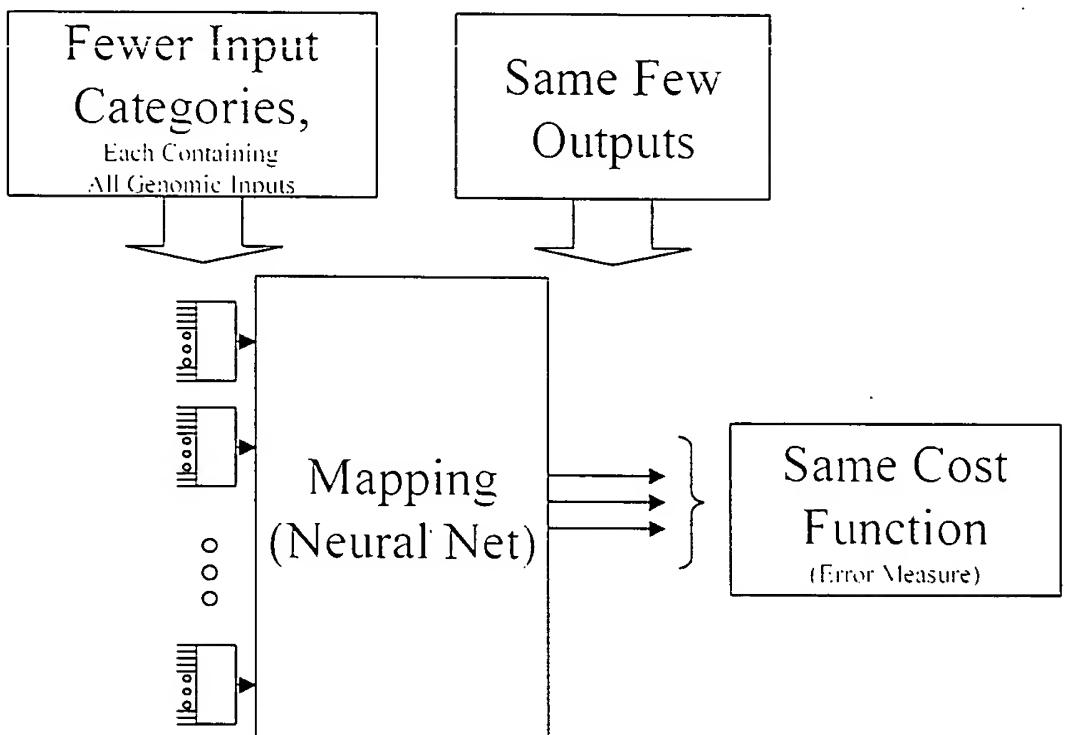


Figure 4D  
GA Rolling: Illustration of the Use of the  
Genetic Algorithm

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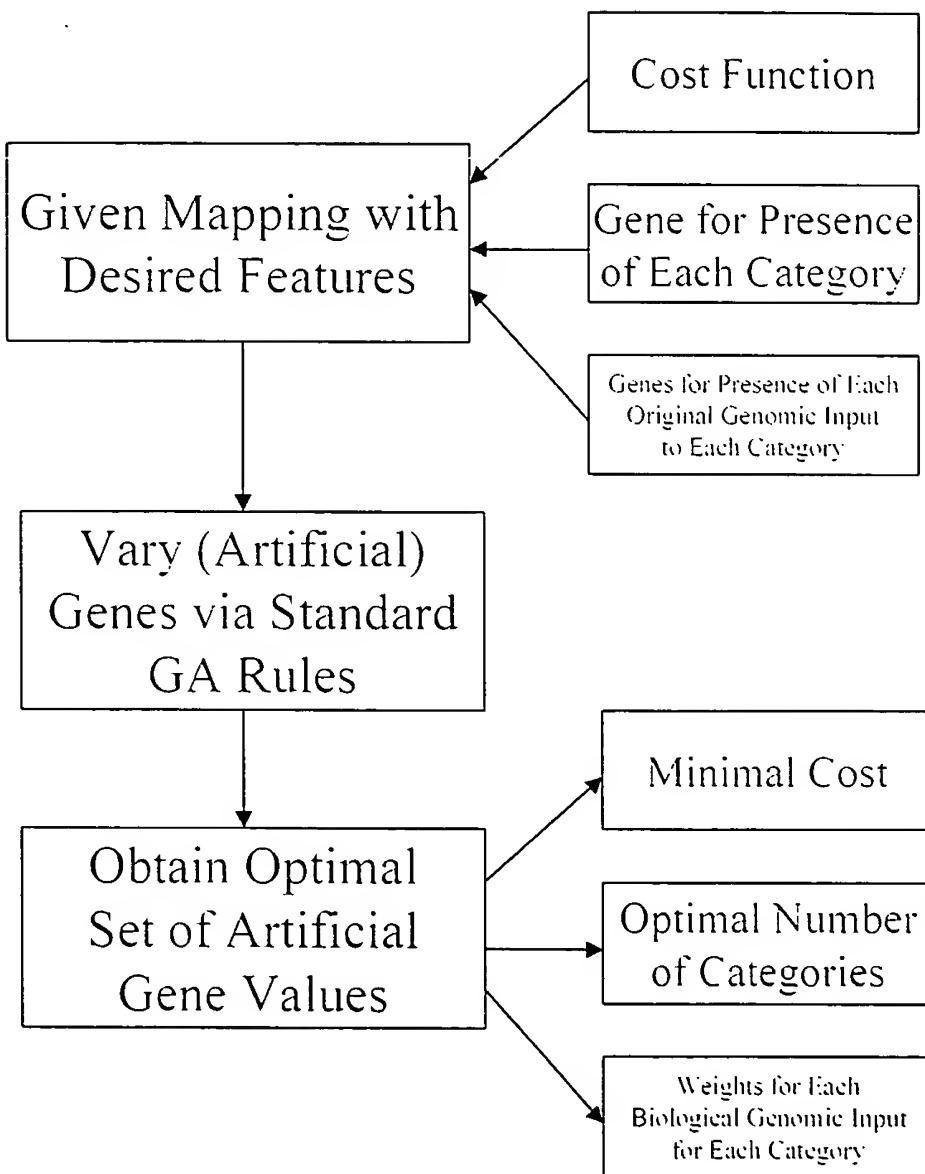


Figure 5A  
Use of Functional Genomic Categorizations for  
Predicting Drug Interactions:  
Preliminary Constructs

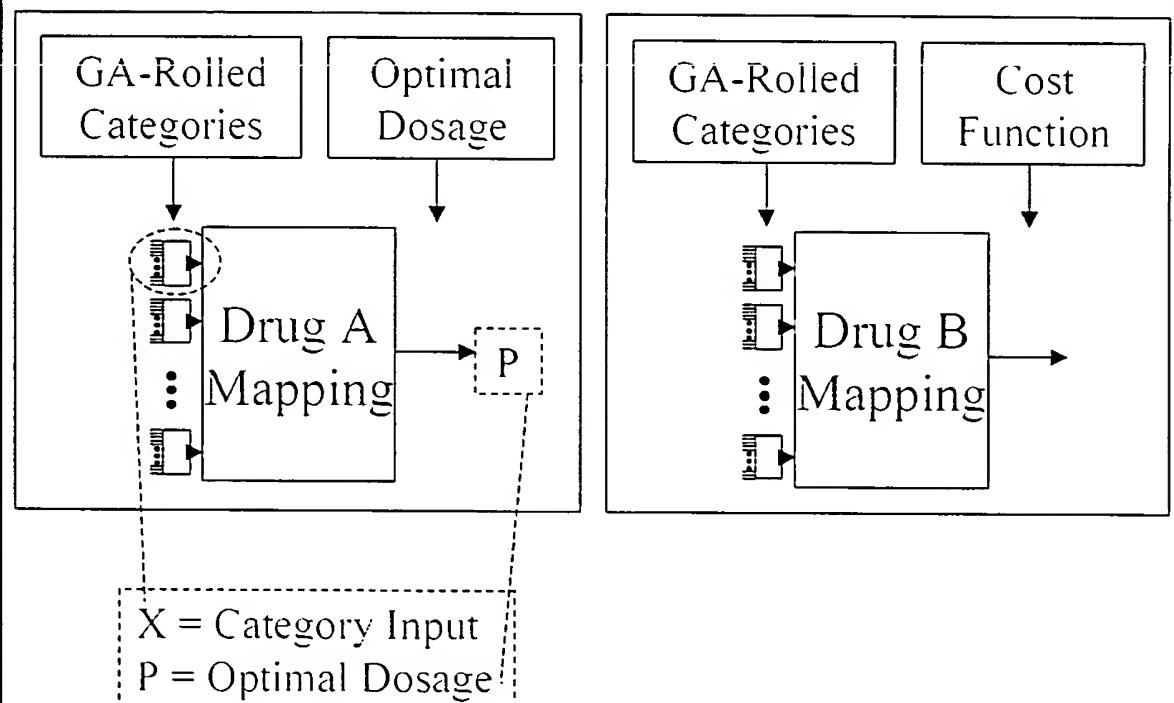


Figure 5B

## Use of Functional Genomic Categorizations for Predicting Drug Interactions: Intermediate Calculations

“Equivalence” of optimal drug dosage  
and category X:

$$E = -\delta(\ln(P)) / \delta(\ln(X))$$

(Roughly in range [-2,2].)

Estimated equivalent of optimal drug dosage  
in units of category X:

$$\delta X_{\text{drug}} \sim E X_{\text{patient}}$$
$$(\delta X_{\text{drug}} = \text{Integral}(0, X_{\text{patient}}) E(X') dX')$$

Model effect of Drug A on Drug B  
with effectively altered genomic inputs  
(to Cost B mapping):

$$X = X_{\text{patient}} + \delta X_{\text{drug}}$$

Identify corresponding increases in Cost B  
as interactions (of A on B) if cost  
increases > e.g. 30%

Figure 6A  
Universal Functional Genomic Categorization:  
Assembly of Categories

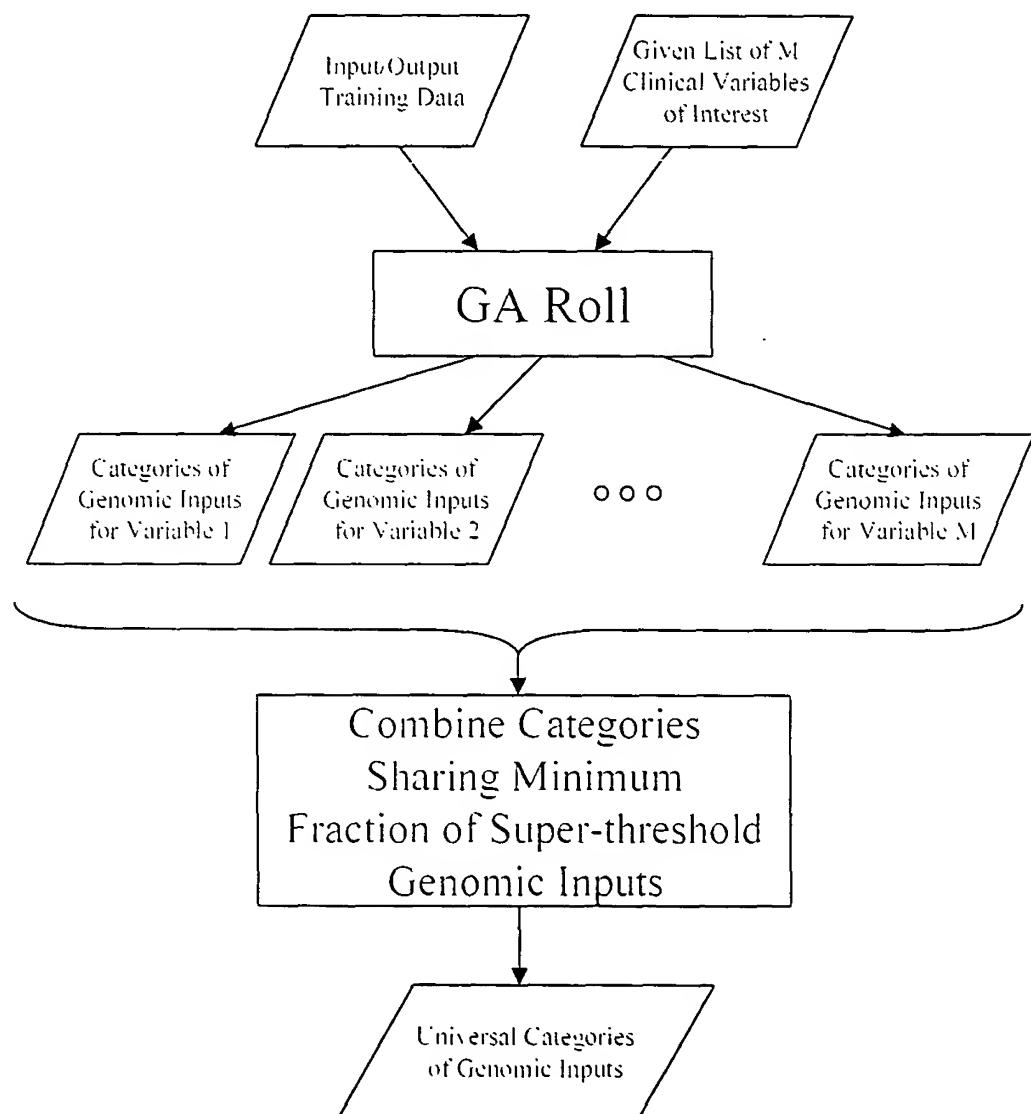


Figure 6B

## Universal Functional Genomic Categorization: Calculation of Probabilities: Given Information

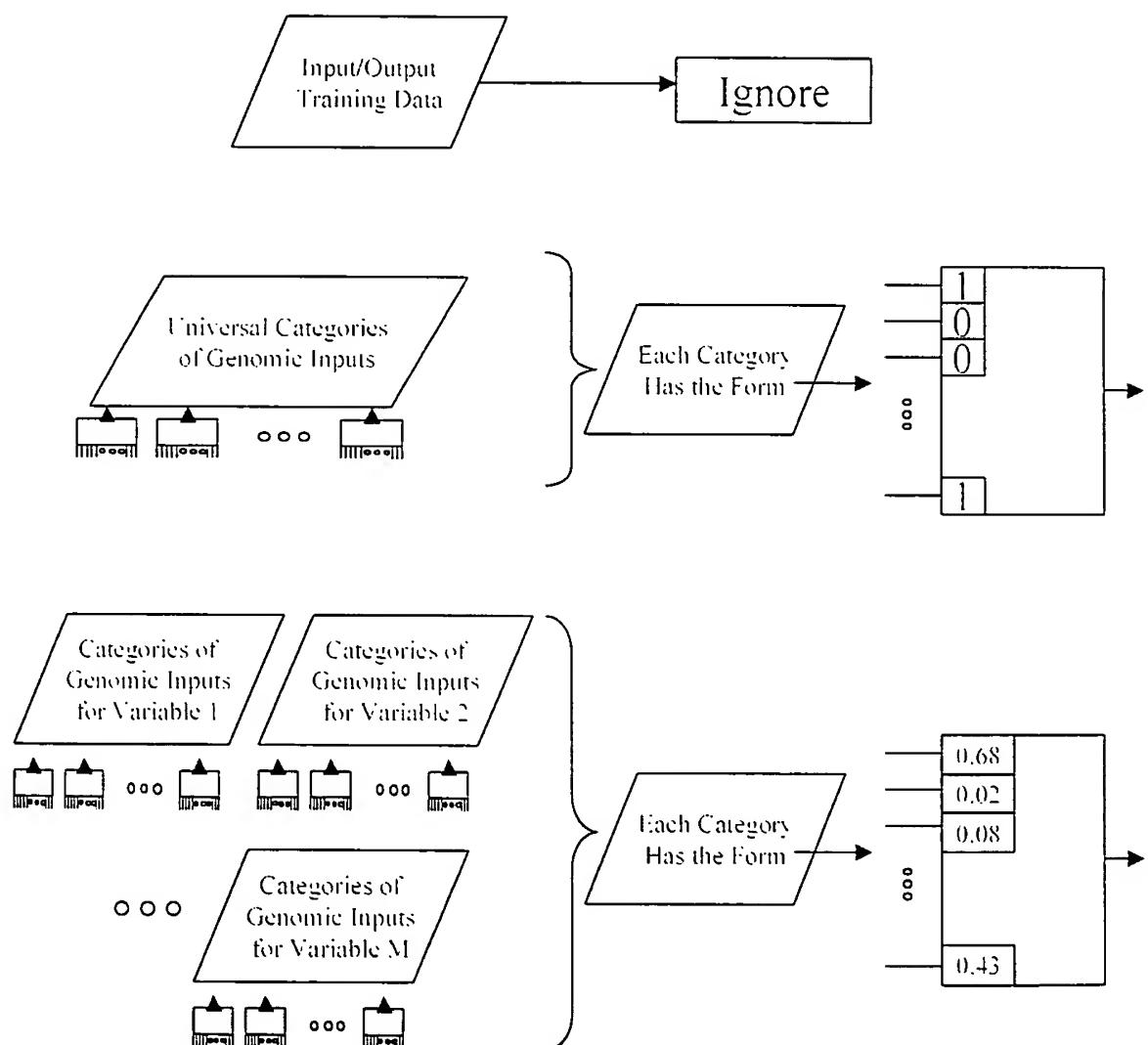


Figure 6C  
 Universal Functional Genomic Categorization:  
 Calculation of Probabilities:  
 Identification of Data

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